



SEQUENCE LISTING

<110> Chang, Chia-Hwa
Liu, Xiaowen
Lewicki, John A.
Xu, Qiang
Osel, Inc.

<120> Surface Expression of Biologically Active Proteins in
Bacteria

<130> 016976-000810US

<140> US 10/766,993

<141> 2004-01-28

<150> US 60/443,619

<151> 2003-01-29

<160> 89

<170> PatentIn Ver. 2.1

<210> 1

<211> 1765

<212> PRT

<213> Lactobacillus jensenii 1153

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<223> genomic C14 cell wall anchor sequence

<220>

<221> DOMAIN

<222> (1528)..(1765)

<223> CWA200 cell wall associated region with anchor
motif

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<221> PEPTIDE

<222> (1730)..(1734)

<223> anchor motif, sorting signal, cell wall targeting
region

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35 40 45

Thr Ile Asn Gly Asn Gly His Arg Ile Asn Phe Ala Gly Tyr Ser Ile
50 55 60

Ala Leu Gln Asn Lys Asn Tyr Thr Asn Ala Ala Asn Pro Trp Asn Ile
65 70 75 80

Thr Leu Lys Asp Met Thr Ile Glu Gly Ser Lys Tyr Asp Tyr Ser Pro
85 90 95

Ile	Ser	Phe	Tyr	Gly	Arg	Lys	Ser	Asn	Thr	Glu	Asn	Ser	Lys	Leu	Thr	100	105	110	
Phe	Asp	Gly	Val	Thr	Ala	Asn	Leu	Asn	Asp	Arg	Pro	Leu	Val	Asp	Lys	115	120	125	
Tyr	Gly	Glu	Asn	Leu	Pro	Val	His	Phe	Ala	Gly	Glu	Asn	Asn	Ile	Thr	130	135	140	
Leu	Asn	Asn	Met	Ser	Ile	Gly	Tyr	Asn	Leu	Val	Thr	Gly	Lys	Thr	Val	145	150	155	160
Lys	Phe	Asp	Ser	Gly	Asn	Thr	Thr	Phe	Asn	Val	Asp	Gly	Lys	Val	Thr	165	170	175	
Gly	Asn	Ser	Ile	Asn	Pro	Asp	Asn	Trp	Val	Ile	Arg	Ser	Thr	Glu	Asn	180	185	190	
Ala	Ser	Asn	Ser	Glu	Asn	Pro	Ser	Thr	Leu	Ile	Asn	Glu	Gly	Ala	Thr	195	200	205	
Val	Thr	Ile	Asn	Ala	Lys	Ser	Asp	Asp	Leu	Arg	Gly	Ile	Tyr	Ala	Gly	210	215	220	
Arg	Gln	Leu	Thr	Ala	Gly	Gln	Pro	Ile	Tyr	Gly	Val	Thr	Val	Ile	Asn	225	230	235	240
Gly	Thr	Leu	Asn	Ala	Lys	Met	Ala	Ala	Gly	His	Ser	Thr	Ala	Ile	Trp	245	250	255	
Ser	His	Asp	Leu	Glu	Ile	Gly	Lys	Lys	Gly	Asn	Val	Thr	Ile	His	Thr	260	265	270	
Lys	Gln	Thr	Asn	Gln	Ala	Asp	Gly	Val	Glu	Asn	Gly	Thr	Ser	Asn	Ser	275	280	285	
Val	Thr	Asn	Tyr	Asn	Gly	Thr	His	Tyr	Ala	Pro	Ile	Ser	Leu	Gly	Val	290	295	300	
Gly	Pro	Ile	Ser	Ser	Val	Ala	Ser	Pro	Leu	Ser	Lys	Gln	Thr	Val	Ser	305	310	315	320
Leu	Ile	Asn	Asn	Gly	Ser	Leu	Thr	Ile	Ile	Arg	Asp	Thr	Ala	Lys	Lys	325	330	335	
Thr	Leu	Val	Pro	Leu	Ile	Ser	Met	Gly	Asp	Gly	Ser	Leu	Ser	Ser	Asn	340	345	350	
Thr	Thr	Leu	Lys	Phe	Ser	Val	Gly	Ala	Gly	Ala	Thr	Leu	Asp	Leu	Gln	355	360	365	
Asp	Lys	Ala	Gly	Thr	Phe	Arg	Tyr	Gly	Ile	Glu	Pro	Ser	Thr	Pro	Leu	370	375	380	
Asn	Gly	Leu	Val	Thr	Leu	Trp	Gly	Thr	Ser	Gly	Thr	Asp	Leu	Leu	Glu	385	390	395	400
Phe	Leu	Thr	Pro	Ala	Tyr	Val	Asn	Leu	Gln	Arg	Thr	Gly	Asp	Ile	Arg	405	410	415	

Gly	Thr	Leu	Ile	Arg	Met	Glu	Gly	Val	Tyr	Asn	Ser	Thr	Thr	Val	Asn	
			420					425						430		
Gly	Pro	Thr	Pro	Val	Ala	Gln	Trp	Asp	Gln	Gly	Asn	Lys	Thr	Thr	Thr	
		435					440					445				
Pro	Asn	Asp	Val	Trp	Tyr	Val	Arg	Tyr	Leu	Ile	Ser	Ala	Asn	Gln	Trp	
	450					455					460					
Gly	Asn	Asn	Ser	Gly	Gln	Phe	Met	Gly	Lys	Asp	Gln	His	Pro	Asn	Thr	
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Val	Val	Ala	Lys	Lys	Gly	Val	Asp	Thr	Leu	Tyr	Asn	Ser	Asn	Ala	Thr	
				485					490						495	
Val	Leu	Met	Ser	Lys	Asn	Gln	Gly	Ala	Asp	Lys	Tyr	Glu	Asn	Gly	Thr	
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	530					535					540					
Asn	Asp	Asn	Pro	Asp	Val	Lys	Ile	Asp	Asp	Phe	Asp	Lys	Tyr	His	Ala	
545					550					555					560	
Glu	Ala	Gln	Thr	Ile	Asp	Gly	Thr	Thr	Arg	Gln	Thr	Leu	Ser	Asp	Leu	
				565					570					575		
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Ile	Thr	Asp	Phe	Lys	Asp	Ile	Val	Lys	His	Val	Thr	Trp	Tyr	Asn	Ser	
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Ser	Lys	Asp	Pro	Ser	Ala	Arg	Val	Pro	Tyr	Pro	Glu	Pro	Gln	Asn	Pro	
625					630					635					640	
Thr	Gly	Asn	Leu	Lys	Thr	Thr	Asp	Gly	Phe	Ala	Trp	Ala	Lys	Val	Thr	
				645					650					655		
Tyr	Ala	Asp	Gly	Ser	Val	Asp	Phe	Val	Lys	Ile	Pro	Leu	Lys	Val	Thr	
			660					665					670			
Glu	Lys	Lys	Tyr	Ser	Glu	Glu	Leu	Thr	Pro	Ser	Tyr	Pro	Gly	Val	Ser	
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Val	Glu	Gln	Gly	Lys	Ser	Asp	Ser	Val	Asp	Pro	Ser	Phe	Lys	Asp	Glu	
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Asn	Asp	Lys	Ala	Ala	Asp	Ala	Pro	Ala	Gly	Thr	Lys	Tyr	Thr	Ala	Gly	
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Glu	Asn	Thr	Pro	Asp	Trp	Ile	Lys	Val	Asp	Pro	Asp	Thr	Gly	Lys	Val	
				725					730					735		

Thr Val Ser Pro Thr Asp Asp Thr Ser Val Gly Ser His Asp Ile Ser
 740 745 750
 Val Thr Val Thr Tyr Pro Asp Ser Ser Thr Asp Gln Leu Thr Val Pro
 755 760 765
 Val Thr Val Thr Glu Lys Ser Asn Leu Ala Glu Lys Tyr Pro Val Ser
 770 775 780
 Tyr Asp Lys Leu Asn Val Glu Lys Pro Ser Gly Asp Thr Pro Ala Thr
 785 790 795 800
 Gly Ala Val Asp Pro Lys Ala Ala Ala Asp Met Pro Glu Gly Ala Ile
 805 810 815
 Thr Gly Tyr Glu Lys Gly Asp Phe Asp Ala Pro Ala Gly Val Thr Ile
 820 825 830
 Asp Val Asn His Asp Thr Gly Lys Val Thr Ala Ser Val Gly Lys Asn
 835 840 845
 Ala Thr Leu Gly Ser Phe Glu Val Pro Val Lys Val Thr Tyr Ser Asp
 850 855 860
 Gly Thr Tyr Ala Glu Val Lys Val Pro Val Ser Ile Thr Gly Asn Lys
 865 870 875 880
 Val Asp Pro Gly Ser Gly Asp Val Val Tyr Tyr Gly Asp Gln Ser Met
 885 890 895
 Val Val Phe Asn Gly Asn Leu Thr Thr Val His Lys Thr Thr Asp Ser
 900 905 910
 His Glu Leu Ser Ala Lys Asp Ser Ala Phe Gln Thr Ile Thr Tyr Tyr
 915 920 925
 Ser Asp Trp Asn Lys Lys Gly Asn Ile Val Ser Asp Tyr Asn Lys His
 930 935 940
 Val Ile Tyr Lys Leu Ser Ala Asp Gly Thr Lys Tyr Val Asn Glu Ala
 945 950 955 960
 Asp Ala Thr Asp Ser Phe Asp Ala Ser Ala Ile Ser Phe Asn Trp Gln
 965 970 975
 Lys Gly Tyr Glu Val Asn Thr Gly Val Asp Asn Phe Ser Asn Gly Ser
 980 985 990
 Ala Asp Thr Leu Tyr Gln Leu Glu Lys Gly Ala Val Asn Ser Glu Glu
 995 1000 1005
 Gln Thr Asp Ala Asn Asp Pro Ser Gly Leu Ala Gly Asn Ser Lys Tyr
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 Arg Tyr Asp Phe Ser Ile Ser Asp Thr Asn Val Leu Gln Lys Leu Gly
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 Leu Ser Pro Ala Gly Tyr Asn Ala Trp Ala Asn Val Tyr Tyr Asn Phe
 1045 1050 1055

Leu Gly Ala Thr Gly Lys Ile Asn Ile Pro Val Asn Tyr Gly Ser Glu
 1060 1065 1070
 Val Ser Thr Asp Glu Ala Gly Ile Lys Asn Tyr Leu Ala Thr Asn Ser
 1075 1080 1085
 Ile Ser Gly Lys Thr Phe Val Asn Gly Asn Pro Thr Gly Ile Lys Trp
 1090 1095 1100
 Ala Glu Asn Gly Met Pro Gly Lys Asp Gly Lys Phe Ala Ala Ser Asn
 1105 1110 1115 1120
 Met Thr Gly Ile Val Glu Phe Thr Phe Asp Asn Gly Thr Lys Leu Asn
 1125 1130 1135
 Val Gln Val Thr Phe Lys Thr Gly Ser His Val Ser Thr Ser Gly Ser
 1140 1145 1150
 Lys Val Asn Asp Asp Thr Asn Leu Tyr Val Glu Arg Thr Ile Glu Tyr
 1155 1160 1165
 Asp Val Thr Gly Thr Gly His Ser Pro Ile Asn Ser Val Thr Gln Lys
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 Val His Tyr Val Arg Asp Gly Tyr His Lys Ile Asn Ala Asp Gly Thr
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 Asp Ala Gly Glu Ile Ile Trp Asn Glu Trp Lys Leu Ala Asp Gly Gln
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 Thr Ala Glu Phe Pro Glu Tyr Ser Val Asp Gln Ile Thr Gly Tyr Asp
 1220 1225 1230
 Ala Tyr Ile Asn Gly Ala Lys Ala Thr Gln Val Asp Ala Ala Lys Val
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 Ala Glu Thr Asn Gly Thr Pro Gln Asn Gly Gln Asn Ile Thr Val Thr
 1250 1255 1260
 Tyr Lys Lys Gln Asn Ser Thr Pro Val Pro Tyr Lys Pro Gly Lys Asp
 1265 1270 1275 1280
 Gly Val Asn Asp Ala Ile Asn Arg Tyr Val Thr Arg Thr Ile Ile Val
 1285 1290 1295
 Lys Glu Pro Gly Lys Glu Pro Gln Thr Ile Thr Gln Thr Val His Phe
 1300 1305 1310
 Thr Asn Glu Asp Lys Asp Gly Asn Ser Gly Tyr Lys Asp Pro Val Thr
 1315 1320 1325
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 1330 1335 1340
 Ala Lys Thr Gly Ser Trp Glu Glu Tyr Thr Ala Pro Ser Val Thr Gly
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 Tyr Thr Pro Ser Gln Ala Lys Val Glu Ala Lys Thr Val Thr Ala Glu
 1365 1370 1375

Thr Glu Ala Ala Ser Val Thr Ile Ser Tyr Thr Lys Asn Ala Asp Ile
 1380 1385 1390
 Pro Val Pro Tyr Lys Pro Gly Lys Asp Gly Val Asn Asp Ala Ile Asn
 1395 1400 1405
 Arg Tyr Val Thr Arg Thr Ile Ile Val Lys Glu Pro Gly Lys Glu Pro
 1410 1415 1420
 Gln Thr Ile Thr Gln Thr Val His Phe Thr Asn Glu Asp Lys Asp Gly
 1425 1430 1435 1440
 Asn Ser Gly Tyr Lys Asp Pro Val Thr Gly Glu Ile Lys Tyr Asn Thr
 1445 1450 1455
 Asp Trp His Val Ala Ser Asp Leu Asn Ala Lys Thr Gly Ser Trp Glu
 1460 1465 1470
 Glu Tyr Thr Ala Pro Ser Val Thr Gly Tyr Thr Pro Ser Gln Ala Lys
 1475 1480 1485
 Val Glu Ala Lys Thr Val Thr Ala Glu Thr Glu Ala Ala Ser Val Thr
 1490 1495 1500
 Ile Ser Tyr Thr Lys Asn Ala Asp Ile Pro Val Pro Phe Asp Pro Ser
 1505 1510 1515 1520
 Asn Lys Asp Met Tyr Arg Glu Val Thr Arg Thr Ile Asn Val Val Asp
 1525 1530 1535
 Pro Ile Thr Gly Lys Ile Ser Thr Ser Val Gln Thr Ala Lys Phe Thr
 1540 1545 1550
 Arg Glu Asp Lys Asn Ser Asn Ala Gly Tyr Thr Asp Pro Val Thr Gly
 1555 1560 1565
 Lys Thr Thr Met Asn Pro Trp Thr Pro Ala Lys Gln Gly Leu Arg Ala
 1570 1575 1580
 Val Asn Val Glu Gln Ile Lys Gly Tyr Val Ala Lys Val Asp Gly Asn
 1585 1590 1595 1600
 Val Asp Ala Val Val Val Thr Pro Asp Ser Ala Asn Met Val Val Thr
 1605 1610 1615
 Ile Thr Tyr Gln Ala Asn Lys Pro Glu Gly Gln Asn Ile Thr Val Lys
 1620 1625 1630
 Lys Asp Thr Val Pro Asp Pro Ala Asp Gly Ile Lys Asn Lys Asp Asp
 1635 1640 1645
 Leu Pro Asp Gly Thr Lys Tyr Thr Trp Lys Glu Val Pro Asp Val Asn
 1650 1655 1660
 Ser Val Gly Glu Lys Thr Gly Ile Val Thr Val Thr Phe Pro Asp Gly
 1665 1670 1675 1680
 Thr Ser Val Asp Val Lys Val Thr Val Tyr Val Asp Pro Val Val Glu
 1685 1690 1695

Ser Asn Arg Asp Thr Leu Ser Lys Glu Ala Asn Thr Gly Asn Thr Asn
1700 1705 1710

Val Ala Lys Ala Ala Thr Val Thr Ser Ser Lys Val Glu Ser Lys Lys
1715 1720 1725

Thr Leu Pro Gln Thr Gly Ser Lys Thr Glu Gln Val Gly Ile Leu Gly
1730 1735 1740

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<213> Lactobacillus jensenii 1153

<220>
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<220>
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<222> (740)..(974)
<223> CWA200 cell wall associated region with anchor motif

<220>
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<222> (941)..(945)
<223> anchor motif, sorting signal, cell wall targeting region

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Gly Ile Val Glu Val Asn Phe Pro Asp Gly Ser Thr Lys Asp Val Pro
35 40 45

Val Glu Val Lys Val Thr Ser Leu Ala Ser Asp Tyr Gln Asn Lys Ile
50 55 60

Asp Thr Lys Gln Ile Ile Ala Lys Tyr Lys Gly Asn Ile Pro Gln Ala
65 70 75 80

Ser Asp Gly Ile Ala Asn Lys Asp Gln Ala Thr Lys Glu Gly Asp Lys
85 90 95

Asp Phe Pro Ser Leu Ala Asp Val Leu Ala Pro Asn Gly Ile Gln Trp
100 105 110

Lys Lys Asn Phe Glu Pro Asp Leu Ser Lys Pro Gly Leu Thr Ser Gly
115 120 125

Glu	Ala	Ile	Leu	Thr	Phe	Lys	Asp	Gly	Ser	Thr	Ala	Glu	Val	Thr	Ile	130	135	140
Pro	Val	Leu	Val	Gln	Thr	Asp	Ala	Asp	Arg	Asn	Thr	Pro	Glu	Thr	Gln	145	150	155
Thr	Ile	Lys	Thr	Leu	Pro	Gly	Gln	Thr	Val	Asn	Pro	Glu	Asp	Gly	Val	165	170	175
Ile	Asn	Leu	His	Lys	Pro	Gly	Glu	Asn	Asn	Pro	Gln	Leu	Pro	Asp	Gly	180	185	190
Thr	Lys	Val	Thr	Phe	Asp	Asn	Gln	Ser	Asp	Val	Asp	Asp	Phe	Thr	Lys	195	200	205
His	Gly	Met	Pro	Gly	Ser	Asp	Lys	Ser	Phe	Asp	Ala	Thr	Val	Thr	Tyr	210	215	220
Pro	Asp	Gly	Thr	Thr	Asp	Lys	Ile	Lys	Leu	Pro	Val	His	Ile	Thr	Ala	225	230	235
Asp	Asn	Glu	Val	Asn	Thr	Pro	Ile	Thr	Gln	Gly	Ile	Ile	Thr	Pro	Lys	245	250	255
Asp	Ser	Val	Pro	Asp	Ala	Asn	Lys	Gly	Ile	Ala	Asn	Leu	Lys	Lys	Ala	260	265	270
Thr	Thr	Lys	Glu	Gly	Lys	Thr	Tyr	Pro	Ala	Leu	Pro	Glu	Asn	Thr	Thr	275	280	285
Val	Glu	Trp	Val	Asn	Pro	Gly	Gln	Met	Lys	Thr	Glu	Leu	Glu	Asn	Ala	290	295	300
Lys	Gly	Gly	Thr	Thr	Lys	Asn	Tyr	Asp	Ala	Val	Val	Ile	Tyr	Pro	Asp	305	310	315
Lys	Ser	Thr	Glu	Ile	Val	Ser	Ile	Pro	Val	Thr	Val	Ala	Thr	Asp	Ala	325	330	335
Asp	Thr	Tyr	Lys	Val	Val	Thr	Gln	Pro	Ile	Asp	Leu	Lys	Asp	Arg	Asn	340	345	350
Leu	Pro	Asp	Asn	Ala	Asp	Asp	Gly	Ile	Thr	Asn	Leu	His	Lys	Pro	Ala	355	360	365
Asp	Phe	Lys	Thr	Pro	Gln	Leu	Pro	Asp	Gly	Thr	His	Ala	Glu	Trp	Gln	370	375	380
Asp	Lys	Asp	Ala	Ala	Gln	Glu	Val	Val	Lys	Asn	Leu	Lys	Pro	Gly	Glu	385	390	395
Thr	Val	Lys	Leu	Pro	Ala	Thr	Val	Val	Phe	Pro	Asp	Gly	Ser	Lys	Lys	405	410	415
Gly	Glu	Gly	Ile	Asp	Val	Ser	Val	His	Leu	His	Gly	Gln	Ser	Asp	Asp	420	425	430
Tyr	Asn	Ile	Glu	Thr	Gln	Pro	Val	Asn	Thr	Asp	Lys	Asp	Gly	Asn	Leu	435	440	445

Pro	Glu	Asn	Ala	Asp	Ser	Gly	Ile	Lys	Asn	Leu	Gly	Lys	Leu	Pro	Glu	450	455	460
Gly	Thr	His	Ala	Ser	Trp	Gly	Asp	Gly	Ala	Gln	Asp	Ile	Ala	Lys	Asn	465	470	475
Leu	Lys	Pro	Gly	Glu	Thr	Lys	Asp	Val	Pro	Ala	Thr	Val	Val	Phe	Pro	485	490	495
Asp	Gly	Ser	Lys	Lys	Glu	Ile	Thr	Ile	Pro	Val	His	Arg	Glu	Gly	Gln	500	505	510
Ser	Asp	Gly	Tyr	Asp	Val	Glu	Pro	Gln	Leu	Val	Asn	Thr	Asp	Lys	Asn	515	520	525
Gly	Gln	Leu	Pro	Asn	Ala	Lys	Glu	Gly	Ile	Lys	Asn	Leu	Ala	Asp	Leu	530	535	540
Pro	Glu	Gly	Thr	Asn	Pro	Thr	Trp	Ala	Asp	Arg	Ala	Gln	Asp	Lys	Ile	545	550	555
Asn	Lys	Thr	Lys	Pro	Gly	Thr	Asp	Thr	Thr	Ala	Gln	Val	Val	Val	Thr	565	570	575
Phe	Pro	Asp	Gly	Ser	Thr	Lys	Glu	Val	Thr	Val	Pro	Val	His	Lys	His	580	585	590
Gly	Gln	Ser	Asp	Asp	Tyr	Gly	Asp	Lys	Ile	Val	Thr	Gln	Arg	Val	Glu	595	600	605
Thr	Asp	Ser	His	Gly	Gln	Leu	Pro	Glu	Asn	Ala	Asp	Ser	Gly	Ile	Lys	610	615	620
Asn	Leu	Gly	Asp	Leu	Pro	Glu	Gly	Thr	His	Ala	Val	Trp	Gly	Gln	Gly	625	630	635
Ala	Gln	Thr	Ile	Val	Asp	Gly	Met	Lys	Pro	Gly	Glu	Thr	Lys	Asp	Val	645	650	655
Pro	Ala	Thr	Ile	Glu	Phe	Pro	Asp	Gly	Ser	Thr	Lys	Asp	Val	Thr	Ile	660	665	670
Pro	Val	Tyr	Lys	Thr	Ser	Thr	Arg	Asp	Gln	Gly	Thr	Leu	Asn	Pro	Pro	675	680	685
Thr	Asp	Lys	Val	Ser	Val	Asp	Asp	Thr	Lys	His	Ile	Thr	Asp	Glu	Asp	690	695	700
Lys	Gly	Lys	Val	Ile	Asp	Asn	Val	Lys	Lys	Ser	Asn	Pro	Asp	Lys	Asp	705	710	715
Ile	Thr	Asp	Ala	His	Val	Asp	Asp	Asp	Gly	Thr	Phe	His	Gly	Lys	Val	725	730	735
Asp	Gly	Gln	Asp	Val	Val	Ile	Pro	Gly	Thr	Glu	Thr	Val	Val	Glu	Lys	740	745	750
Gln	Lys	Glu	Ser	Leu	Asn	Pro	Pro	Thr	Asp	Lys	Val	Pro	Val	Asp	Asp	755	760	765

Thr	Lys	His	Ile	Thr	Asp	Glu	Asp	Lys	Gly	Lys	Val	Ile	Asp	Asn	Val	
770						775					780					
Lys	Lys	Ser	Asn	Pro	Asp	Lys	Asp	Ile	Thr	Asp	Ala	His	Val	Asp	Asp	
785					790					795					800	
Asp	Gly	Thr	Phe	His	Gly	Lys	Val	Asp	Gly	Gln	Asp	Val	Val	Ile	Pro	
			805						810					815		
Gly	Thr	Glu	Thr	Val	Val	Glu	Lys	Gln	Lys	Glu	Ser	Leu	Asn	Pro	Pro	
			820					825					830			
Thr	Asp	Lys	Val	Pro	Val	Asp	Asp	Thr	Lys	His	Ile	Thr	Asp	Glu	Asp	
		835					840					845				
Lys	Gly	Lys	Val	Ile	Asp	Asn	Val	Lys	Lys	Ser	Asn	Pro	Asp	Lys	Asp	
	850					855					860					
Ile	Thr	Asp	Ala	His	Val	Asp	Asp	Asp	Gly	Thr	Phe	His	Gly	Lys	Val	
865					870					875					880	
Asp	Gly	Gln	Asp	Val	Val	Ile	Pro	Gly	Ile	Glu	Thr	Val	Val	Glu	Lys	
			885						890					895		
Ser	Thr	Asn	Asn	Gln	Lys	Ser	Asp	Thr	Asn	Lys	Gly	Leu	Ile	Ser	Asn	
			900					905					910			
Asp	Asn	Ser	Glu	Lys	Asn	Ser	His	Met	Ile	Asn	Ala	Asn	Val	Asn	Thr	
		915					920					925				
Lys	Ser	Arg	Asn	Ser	Leu	Ser	Ala	Lys	Gln	Asn	Arg	Leu	Pro	Gln	Thr	
	930					935					940					
Gly	Ser	Glu	Thr	Ser	Gly	Leu	Ser	Ala	Leu	Gly	Leu	Ala	Met	Leu	Ser	
945					950					955					960	
Leu	Val	Gly	Leu	Gly	Phe	Leu	Ile	Lys	Lys	Arg	Lys	Glu	Asp			
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 <212> PRT
 <213> Lactobacillus jensenii 1153

<220>
 <223> genomic C370 cell wall anchor sequence

<220>
 <221> DOMAIN
 <222> (1309)..(1903)
 <223> CWA200 cell wall associated region with anchor motif

<220>
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 <222> (1868)..(1872)
 <223> anchor motif, sorting signal, cell wall targeting region

<400> 3

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Ser	Asn	Glu	Val	Pro	Gly	Ala	Thr	Asn	Val	Trp	Thr	Ser	Gly	Val	Leu	35	40	45	
Thr	Thr	Gln	Asn	Gly	Pro	Ile	Arg	Ala	Ala	Leu	Ala	Gly	Ser	Thr	Ser	50	55	60	
Ser	Thr	Tyr	Lys	Ile	Tyr	Leu	Lys	Ala	Asp	Thr	Pro	Asn	Ser	Ile	Leu	65	70	75	80
Ser	Lys	Pro	Leu	Ser	Phe	Thr	Met	Trp	Ala	Arg	Tyr	Ser	Ser	Gly	His	85	90	95	
Asp	Met	Val	Ser	Asp	Phe	Ser	Lys	Asn	Leu	Ile	Leu	Asn	Asp	Asn	Glu	100	105	110	
Thr	Thr	Thr	Phe	Ser	Ser	Asn	Asn	Phe	Phe	Lys	Ser	Leu	Asp	Ile	Val	115	120	125	
Asn	Asn	Asp	Gly	Pro	Ile	Leu	Asp	Asn	Met	Ser	Val	Asp	Tyr	Ser	Asn	130	135	140	
Lys	Thr	Val	Asn	Thr	Arg	Tyr	Arg	Val	Asn	Gly	Ser	Leu	Leu	Gly	Asp	145	150	155	160
Lys	Ser	Asn	Leu	Thr	Leu	Arg	Ile	Arg	Gly	Asn	Asp	Asn	Leu	Leu	Lys	165	170	175	
Leu	Ile	Asp	Lys	Val	Lys	Ile	Ser	Asn	Lys	Thr	Tyr	Thr	Leu	Ala	Asn	180	185	190	
Asn	Thr	Leu	Lys	Tyr	Arg	Thr	Gly	Glu	Leu	Tyr	Ile	Asn	Asp	Ile	Gly	195	200	205	
Gly	Ser	Leu	Gly	Phe	Leu	Ser	Ser	Leu	Ser	Asn	Arg	Gln	Asp	Phe	Asn	210	215	220	
Val	Thr	Phe	Tyr	Leu	Lys	Asn	Gly	Lys	Ser	Phe	Ala	Asp	Ala	Leu	Thr	225	230	235	240
Ser	Glu	Ser	Gln	Lys	Phe	Asp	Phe	Gln	Phe	Gly	Ile	Tyr	Asp	Thr	Thr	245	250	255	
Asp	Tyr	Ala	Thr	Ala	Phe	His	Ser	Leu	Asp	Thr	Val	Thr	Asn	Ser	Leu	260	265	270	
Ser	Thr	Lys	Thr	Tyr	Thr	Thr	Gly	Asp	Lys	Tyr	Asn	Asn	Gln	Thr	Tyr	275	280	285	
Asp	Leu	Ser	Thr	Phe	Lys	Thr	Ile	Leu	Asp	Lys	Leu	Ile	Lys	Gln	Lys	290	295	300	
Gln	Asp	Asn	Pro	Thr	Thr	Tyr	Leu	Ser	Phe	Glu	Asp	Lys	Lys	Ile	Ser	305	310	315	320

Ala	Thr	Glu	Asn	Asn	Pro	Tyr	Glu	Ala	Val	Lys	Leu	Ala	Leu	Glu	Ser	
				325					330					335		
Pro	Thr	Phe	Thr	Asn	Ile	Ser	Ile	Ala	Lys	Ser	Leu	Val	Asn	Ala	Ala	
			340					345					350			
Asp	Cys	Lys	Gln	Leu	Asp	Asn	Thr	Ala	Lys	Trp	Ala	Trp	Asp	Asn	Gly	
		355					360					365				
Ala	Arg	Asp	Asp	Leu	Leu	Lys	Tyr	Leu	Asp	Val	Ala	Thr	Lys	Val	Ala	
	370					375					380					
Ser	Tyr	Ile	His	Leu	Glu	Phe	Pro	Thr	Lys	Pro	Thr	Asp	Phe	Ser	Gly	
385					390					395					400	
Leu	Leu	Leu	Arg	Tyr	Thr	Arg	Ala	Gly	Thr	Phe	Ile	Ser	Ala	Val	Asp	
			405						410					415		
Ser	Asp	Arg	Asp	Gly	Val	Leu	Asp	Ile	Thr	Glu	Ile	Asp	Asn	Ser	Tyr	
			420					425					430			
Gly	Met	Asn	Pro	Ser	Val	Tyr	Asp	Thr	Asp	Gly	Asp	Gly	Ile	Ser	Asp	
		435					440					445				
Gly	Gln	Glu	Leu	Arg	Glu	Gly	Arg	Asp	Pro	Gly	Val	Ala	Pro	Phe	Asn	
	450					455					460					
Trp	Thr	Asp	Ala	Asn	Gly	Asn	Gln	Leu	Ser	Ile	Asp	Val	Asp	Thr	Thr	
465					470					475					480	
Thr	Ile	Ser	Gly	Gln	Leu	Gly	Asn	His	Asn	Tyr	His	Asn	Glu	Val	Met	
				485					490					495		
Gln	Pro	Arg	Thr	Val	Asn	Leu	Tyr	Lys	Val	Asp	Asp	Thr	Gly	Lys	Lys	
			500					505					510			
Thr	Leu	Ile	Ala	Tyr	Thr	Thr	Ser	Ala	Val	Asp	Gln	Asn	Gly	Ser	Phe	
		515					520					525				
Thr	Leu	Ser	Lys	Phe	Thr	Leu	Asn	Lys	Gly	Asp	Lys	Leu	Val	Ile	Gly	
	530					535					540					
Tyr	Val	Thr	Pro	Arg	Thr	Asn	Lys	Ser	Leu	Thr	Asp	Lys	Asp	Thr	Ile	
545					550					555					560	
Leu	Gln	Gln	Ala	Phe	Pro	Thr	Glu	Gln	Phe	Ser	Asn	Glu	Ile	Ile	Val	
				565					570					575		
Lys	Gly	Lys	Gln	Val	Thr	Val	Thr	Phe	Asn	Met	Asn	Gly	Val	Ser	Asp	
			580					585					590			
Asp	Glu	Asn	Gln	Asp	Ile	Lys	Val	Glu	Lys	Asp	Ser	Ser	Phe	Asn	Lys	
		595					600					605				
Asp	Ser	Leu	Thr	Leu	Pro	Thr	Pro	Thr	Met	Lys	Thr	Gly	Tyr	Ser	Phe	
	610					615					620					
Lys	Glu	Trp	Asn	Thr	Gln	Ala	Asp	Gly	Lys	Gly	Thr	Val	Val	Thr	Ala	
625					630					635					640	

Asp	Thr	Ile	Phe	Asp	Thr	Asp	Thr	Thr	Val	Tyr	Ala	Ile	Gly	Glu	Lys	
				645					650					655		
Ile	Lys	Leu	Pro	Asn	Pro	Thr	Asn	Ile	Lys	Ala	Glu	Thr	Arg	Thr	Asp	
			660					665					670			
Asp	Lys	Thr	Lys	Ser	Gln	Glu	Thr	Ile	Ile	Thr	Gly	Lys	Ala	Thr	Pro	
		675					680					685				
Gly	Ala	Thr	Val	Thr	Ile	Lys	Asp	Asn	Leu	Gly	Asn	Glu	Ile	Gly	Thr	
	690					695					700					
Gly	Val	Ala	Asn	Asp	Ala	Gly	Asn	Phe	Glu	Ile	Lys	Thr	Thr	Ser	Pro	
705					710					715					720	
Leu	Ala	Glu	Ala	Thr	Lys	Val	Ser	Val	Glu	Ala	Thr	Lys	Gly	Gly	Glu	
				725					730					735		
Ser	Ser	Asp	Ala	Val	Glu	Ala	Thr	Val	Glu	Gln	Asn	Asn	Phe	Gln	Lys	
			740					745					750			
Gly	Asn	Pro	Leu	Ile	Gln	Pro	Ala	Ser	Pro	Thr	Ala	Val	Thr	Ala	Val	
		755					760						765			
Thr	Ile	Lys	Ala	Ser	Asp	Gly	Thr	Asn	Asn	Ser	Thr	Thr	Val	Thr	Gly	
	770					775						780				
Lys	Ala	Ala	Ala	Gly	Glu	Thr	Val	Thr	Val	Lys	Asp	Ser	Ser	Gly	Asn	
785					790					795					800	
Glu	Ile	Gly	Thr	Gly	Val	Val	Gly	Glu	Asp	Gly	Thr	Phe	Thr	Ile	Thr	
				805					810					815		
Thr	Asn	Lys	Pro	Ile	Ala	Glu	Asn	Glu	Arg	Ile	Gln	Val	Val	Val	Thr	
			820					825					830			
Lys	Asp	Asp	Ala	Glu	Ser	Glu	Pro	Thr	Glu	Ala	Val	Val	Thr	Ala	Lys	
			835				840					845				
Thr	Glu	Pro	Thr	Asn	Pro	Thr	Glu	Val	Thr	Ala	Lys	Thr	Leu	Pro	Asp	
	850					855						860				
Gly	Asn	Ser	Asp	Ser	Thr	Ile	Val	Ala	Gly	Lys	Gly	Lys	Ala	Gly	Glu	
865					870					875					880	
Val	Val	Thr	Val	Lys	Asn	Asp	Ala	Gly	Lys	Val	Ile	Gly	Thr	Gly	Lys	
				885					890					895		
Val	Ser	Asp	Asp	Gly	Thr	Phe	Ser	Ile	Lys	Thr	Asp	Glu	Val	Ile	Glu	
			900					905					910			
Pro	Gly	Lys	Gln	Val	Ser	Val	Ile	Thr	Thr	Asn	Asp	Gly	Met	Asp	Ser	
		915					920					925				
Ile	Pro	Val	Pro	Val	Thr	Val	Ser	Gly	Glu	Thr	Ile	Thr	Ser	Ile	Lys	
	930					935						940				
Gln	Ser	Ala	Lys	Ala	Ala	Val	Asp	Asn	Leu	Thr	Tyr	Leu	Asn	Asn	Ala	
945					950					955					960	

Gln Lys Gln Ser Ala Lys Asp Ala Ile Asp Ser Ala Asn Thr Val Asp
 965 970 975

Glu Ile Thr Thr Ala Lys Asn Asn Ala Val Ser Thr Asp Thr Asn Met
 980 985 990

Lys Asp Leu Ser Glu Asp Thr Lys Leu Ala Ala Asp Lys Thr Gln Asp
 995 1000 1005

Pro Tyr Leu Asn Ala Asp Leu Asp Lys Lys Gln Ala Tyr Asp Lys Ala
 1010 1015 1020

Val Glu Glu Ala Gln Lys Leu Leu Asn Lys Glu Thr Gly Thr Ser Val
 1025 1030 1035 1040

Gly Ala Asp Lys Asp Pro Ala Glu Val Ala Arg Ile Lys Gln Ala Val
 1045 1050 1055

Asp Asp Ala Tyr Asp Ala Leu Asn Gly Asn Ser Ser Leu Asp Asp Ala
 1060 1065 1070

Lys Gln Lys Ala Lys Asp Ala Val Asp Lys Asn Tyr Thr Asn Leu Asn
 1075 1080 1085

Asp Lys Gln Lys Glu Thr Ala Lys Lys Arg Ile Asp Ser Ala Lys Ser
 1090 1095 1100

Glu Asp Glu Val Asn Asn Ala Asp Lys Ile Asn Ser Gly Leu Asn Glu
 1105 1110 1115 1120

Lys Met Gly Glu Leu Lys Glu Val Ser Asn Leu Ser Asp Lys Ile Glu
 1125 1130 1135

Thr Thr Ser Asn Tyr Ser Asn Ala Asp Ser Asp Lys Lys Gln Ala Tyr
 1140 1145 1150

Lys Glu Thr Ala Asp Lys Ile His Glu Thr Val Ala Pro Ser Gly Asp
 1155 1160 1165

Asp Leu Thr Thr Asp Asp Val Asn Asn Leu Ile Thr Asp Glu Ala Thr
 1170 1175 1180

Lys Arg Ala Ala Leu Asn Gly Asp Ala Arg Glu Lys Ala Arg Gln Glu
 1185 1190 1195 1200

Leu Glu Asn Asn Tyr Asn Ser Gly Lys Ser Leu Gln Asp Gly Ser Thr
 1205 1210 1215

Leu Asp Pro Arg Tyr Tyr Asn Ala Ser Glu Glu Lys Lys Gln Ala Phe
 1220 1225 1230

Gln Lys Ala Leu Asp Asn Ala Lys Lys Ala Leu Asp Asn Ser Glu Thr
 1235 1240 1245

Thr Glu Ala Glu Tyr Lys Ser Ala Asn Asp Glu Leu Gln Lys Ala Lys
 1250 1255 1260

Ala Asp Leu Asp Gly Gln Thr Thr Asp Lys Ser Lys Leu Asp Asp Ala
 1265 1270 1275 1280

Ile Lys Asp Ala Asn Asn Ala Lys Gly Thr Asp Lys Tyr Lys Asn Ala
 1285 1290 1295
 Ser Asp Asp Thr Lys Ser Lys Phe Asp Glu Ala Leu Lys Lys Ala Glu
 1300 1305 1310
 Glu Val Lys Asn Asn Ser Asn Ala Thr Gln Lys Glu Val Asp Asp Ala
 1315 1320 1325
 Thr Asn Asn Leu Lys Gln Ala Gln Asn Asn Leu Asn Gly Gln Thr Thr
 1330 1335 1340
 Asp Lys Ser Lys Leu Asp Asp Ala Ile Lys Asp Ala Asn Asn Ala Lys
 1345 1350 1355 1360
 Gly Thr Asp Lys Tyr Lys Asn Ala Ser Asp Asp Thr Lys Ser Lys Phe
 1365 1370 1375
 Asp Asp Ala Leu Lys Lys Ala Glu Glu Val Lys Asn Asn Ser Asn Ala
 1380 1385 1390
 Thr Gln Lys Glu Val Asp Asp Ala Thr Asn Asn Leu Lys Gln Ala Gln
 1395 1400 1405
 Asn Asp Leu Asp Gly Gln Thr Thr Asp Lys Ser Lys Leu Asp Glu Ala
 1410 1415 1420
 Ile Thr Asp Ala Asn Asn Thr Lys Leu Thr Asp Lys Tyr Asn Asn Ala
 1425 1430 1435 1440
 Ser Asp Asp Thr Lys Ser Lys Phe Asp Glu Ala Leu Lys Lys Ala Glu
 1445 1450 1455
 Asn Val Lys Asn Asp Ser Asn Ala Thr Gln Lys Glu Val Asp Asp Ala
 1460 1465 1470
 Thr Asn Asn Leu Lys Gln Ala Gln Asn Asp Leu Asp Gly Gln Thr Thr
 1475 1480 1485
 Asp Lys Ser Lys Leu Asp Glu Ala Ile Thr Asp Ala Asn Asn Thr Lys
 1490 1495 1500
 Ser Thr Asp Lys Tyr Asn Asn Ala Ser Asp Asp Thr Lys Ser Lys Phe
 1505 1510 1515 1520
 Asp Glu Ala Leu Lys Lys Ala Glu Glu Val Lys Asn Asn Ser Asn Ala
 1525 1530 1535
 Thr Gln Lys Glu Val Asp Asp Ala Thr Asn Asn Leu Lys Gln Ala Gln
 1540 1545 1550
 Asn Asn Leu Asp Gly Gln Thr Thr Asp Lys Ser Lys Leu Asp Glu Ala
 1555 1560 1565
 Ile Thr Asp Ala Asn Asn Thr Lys Ser Thr Asp Lys Tyr Lys Asn Ala
 1570 1575 1580
 Ser Asp Asp Thr Lys Ser Lys Phe Asp Asp Ala Leu Lys Lys Ala Glu
 1585 1590 1595 1600

Glu Val Lys Asn Asn Ser Asn Ala Thr Gln Lys Glu Val Asp Asp Ala
 1605 1610 1615
 Thr Asn Asn Leu Lys Gln Ala Gln Asn Asp Leu Asp Gly Gln Thr Thr
 1620 1625 1630
 Asn Lys Asp Thr Leu Asn Asp Ala Ile Lys Asp Ala Asn Asp Ala Lys
 1635 1640 1645
 Gly Thr Asp Lys Tyr Lys Asn Ala Ser Asp Asp Thr Lys Ser Lys Leu
 1650 1655 1660
 Asp Glu Thr Leu Lys Lys Ala Glu Glu Val Lys Asn Asn Ser Asn Ala
 1665 1670 1675 1680
 Thr Gln Lys Glu Val Asp Asp Ala Thr Asn Asn Leu Lys Gln Ala Gln
 1685 1690 1695
 Asn Asp Leu Asp Gly Gln Thr Thr Asp Lys Ser Lys Leu Asp Glu Ala
 1700 1705 1710
 Ile Lys Ser Ala Asp Asp Thr Lys Ser Thr Asp Lys Tyr Asn Asn Ala
 1715 1720 1725
 Ser Asp Asp Thr Lys Ser Lys Phe Asp Glu Ala Leu Lys Lys Ala Glu
 1730 1735 1740
 Glu Val Lys Asn Asn Ser Asn Ala Thr Gln Lys Glu Val Asp Asp Ala
 1745 1750 1755 1760
 Thr Lys Asn Leu Lys Gln Ala Gln Asn Asp Leu Asp Gly Gln Thr Thr
 1765 1770 1775
 Asn Lys Asp Ala Ile Asn Asp Ala Ile Lys Asp Ala Asn Asn Ala Lys
 1780 1785 1790
 Gly Thr Asp Lys Tyr Asn Asn Ala Ser Asp Asp Thr Lys Ser Lys Phe
 1795 1800 1805
 Asp Asp Ala Leu Lys Lys Ala Glu Asp Val Lys Asn Asp Ser Asn Ala
 1810 1815 1820
 Asn Gln Lys Glu Val Asp Asp Ala Thr Lys Asn Leu Lys Asn Thr Leu
 1825 1830 1835 1840
 Asn Asn Leu Lys Gly Gln Pro Ala Lys Lys Ala Asn Leu Ile Ala Ser
 1845 1850 1855
 Lys Asp Asn Ala Lys Ile His Lys Gln Thr Leu Leu Pro Gln Thr Gly
 1860 1865 1870
 Thr Glu Thr Asn Pro Leu Thr Ala Ile Gly Ile Gly Leu Met Ala Leu
 1875 1880 1885
 Gly Ala Gly Ile Phe Ala Lys Lys Lys Arg Lys Asp Asp Glu Ala
 1890 1895 1900

<210> 4
 <211> 199
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C370 cell wall
 associated (CWA) region

<400> 4
 Lys Lys Ala Glu Glu Val Lys Asn Asn Ser Asn Ala Thr Gln Lys Glu
 1 5 10 15
 Val Asp Asp Ala Thr Asn Asn Leu Lys Gln Ala Gln Asn Asp Leu Asp
 20 25 30
 Gly Gln Thr Thr Asp Lys Ser Lys Leu Asp Glu Ala Ile Lys Ser Ala
 35 40 45
 Asp Asp Thr Lys Ser Thr Asp Lys Tyr Asn Asn Ala Ser Asp Asp Thr
 50 55 60
 Lys Ser Lys Phe Asp Glu Ala Leu Lys Lys Ala Glu Glu Val Lys Asn
 65 70 75 80
 Asn Ser Asn Ala Thr Gln Lys Glu Val Asp Asp Ala Thr Lys Asn Leu
 85 90 95
 Lys Gln Ala Gln Asn Asp Leu Asp Gly Gln Thr Thr Asn Lys Asp Ala
 100 105 110
 Ile Asn Asp Ala Ile Lys Asp Ala Asn Asn Ala Lys Gly Thr Asp Lys
 115 120 125
 Tyr Asn Asn Ala Ser Asp Asp Thr Lys Ser Lys Phe Asp Asp Ala Leu
 130 135 140
 Lys Lys Ala Glu Asp Val Lys Asn Asp Ser Asn Ala Asn Gln Lys Glu
 145 150 155 160
 Val Asp Asp Ala Thr Lys Asn Leu Lys Asn Thr Leu Asn Asn Leu Lys
 165 170 175
 Gly Gln Pro Ala Lys Lys Ala Asn Leu Ile Ala Ser Lys Asp Asn Ala
 180 185 190
 Lys Ile His Lys Gln Thr Leu
 195

<210> 5
 <211> 95
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C370 cell wall
 associated fragment

<400> 5
 Gly Gln Thr Thr Asn Lys Asp Ala Ile Asn Asp Ala Ile Lys Asp Ala
 1 5 10 15
 Asn Asn Ala Lys Gly Thr Asp Lys Tyr Asn Asn Ala Ser Asp Asp Thr
 20 25 30
 Lys Ser Lys Phe Asp Asp Ala Leu Lys Lys Ala Glu Asp Val Lys Asn
 35 40 45
 Asp Ser Asn Ala Asn Gln Lys Glu Val Asp Asp Ala Thr Lys Asn Leu
 50 55 60
 Lys Asn Thr Leu Asn Asn Leu Lys Gly Gln Pro Ala Lys Lys Ala Asn
 65 70 75 80
 Leu Ile Ala Ser Lys Asp Asn Ala Lys Ile His Lys Gln Thr Leu
 85 90 95

<210> 6
 <211> 202
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C14 cell wall
 associated (CWA) region

<400> 6
 Val Thr Arg Thr Ile Asn Val Val Asp Pro Ile Thr Gly Lys Ile Ser
 1 5 10 15
 Thr Ser Val Gln Thr Ala Lys Phe Thr Arg Glu Asp Lys Asn Ser Asn
 20 25 30
 Ala Gly Tyr Thr Asp Pro Val Thr Gly Lys Thr Thr Met Asn Pro Trp
 35 40 45
 Thr Pro Ala Lys Gln Gly Leu Arg Ala Val Asn Val Glu Gln Ile Lys
 50 55 60
 Gly Tyr Val Ala Lys Val Asp Gly Asn Val Asp Ala Val Val Val Thr
 65 70 75 80
 Pro Asp Ser Ala Asn Met Val Val Thr Ile Thr Tyr Gln Ala Asn Lys
 85 90 95
 Pro Glu Gly Gln Asn Ile Thr Val Lys Lys Asp Thr Val Pro Asp Pro
 100 105 110
 Ala Asp Gly Ile Lys Asn Lys Asp Asp Leu Pro Asp Gly Thr Lys Tyr
 115 120 125
 Thr Trp Lys Glu Val Pro Asp Val Asn Ser Val Gly Glu Lys Thr Gly
 130 135 140
 Ile Val Thr Val Thr Phe Pro Asp Gly Thr Ser Val Asp Val Lys Val
 145 150 155 160

Thr Val Tyr Val Asp Pro Val Val Glu Ser Asn Arg Asp Thr Leu Ser
165 170 175

Lys Glu Ala Asn Thr Gly Asn Thr Asn Val Ala Lys Ala Ala Thr Val
180 185 190

Thr Ser Ser Lys Val Glu Ser Lys Lys Thr
195 200

<210> 7

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:C14 cell wall
targeting region

<400> 7

Val Thr Arg Thr Ile Asn Val Val Asp Pro Ile Thr Gly Lys Ile Ser
1 5 10 15

Thr Ser Val Gln Thr Ala Lys Phe Thr Arg Glu Asp Lys Asn Ser Asn
20 25 30

Ala Gly Tyr Thr Asp Pro Val Thr Gly Lys Thr Thr Met Asn Pro Trp
35 40 45

Thr Pro Ala Lys Gln Gly Leu Arg Ala Val Asn Val Glu Gln Ile Lys
50 55 60

Gly Tyr Val Ala Lys Val Asp Gly Asn Val Asp Ala Val Val Val Thr
65 70 75 80

Pro Asp Ser Ala Asn Met Val Val Thr Ile Thr Tyr Gln Ala Asn Lys
85 90 95

Pro Glu Gly Gln Asn Ile Thr Val Lys Lys Asp Thr Val Pro Asp Pro
100 105 110

Ala Asp Gly Ile Lys Asn Lys Asp Asp Leu Pro Asp Gly Thr Lys Tyr
115 120 125

Thr Trp Lys Glu Val Pro Asp Val Asn Ser Val Gly Glu Lys Thr Gly
130 135 140

Ile Val Thr Val Thr Phe Pro Asp Gly Thr Ser Val Asp Val Lys Val
145 150 155 160

Thr Val Tyr Val Asp Pro Val Val Glu Ser Asn Arg Asp Thr Leu Ser
165 170 175

Lys Glu Ala Asn Thr Gly Asn Thr Asn Val Ala Lys Ala Ala Thr Val
180 185 190

Thr Ser Ser Lys Val Glu Ser Lys Lys Thr Leu Pro Gln Thr Gly Ser
195 200 205

Lys Thr Glu Gln Val Gly Ile Leu Gly Leu Ala Ile Ala Thr Val Gly
 210 215 220

Ser Leu Leu Gly Leu Gly Val Asn
 225 230

<210> 8
 <211> 226
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C370 cell wall
 targeting region

<400> 8
 Lys Lys Ala Glu Glu Val Lys Asn Asn Ser Asn Ala Thr Gln Lys Glu
 1 5 10 15

Val Asp Asp Ala Thr Asn Asn Leu Lys Gln Ala Gln Asn Asp Leu Asp
 20 25 30

Gly Gln Thr Thr Asp Lys Ser Lys Leu Asp Glu Ala Ile Lys Ser Ala
 35 40 45

Asp Asp Thr Lys Ser Thr Asp Lys Tyr Asn Asn Ala Ser Asp Asp Thr
 50 55 60

Lys Ser Lys Phe Asp Glu Ala Leu Lys Lys Ala Glu Glu Val Lys Asn
 65 70 75 80

Asn Ser Asn Ala Thr Gln Lys Glu Val Asp Asp Ala Thr Lys Asn Leu
 85 90 95

Lys Gln Ala Gln Asn Asp Leu Asp Gly Gln Thr Thr Asn Lys Asp Ala
 100 105 110

Ile Asn Asp Ala Ile Lys Asp Ala Asn Asn Ala Lys Gly Thr Asp Lys
 115 120 125

Tyr Asn Asn Ala Ser Asp Asp Thr Lys Ser Lys Phe Asp Asp Ala Leu
 130 135 140

Lys Lys Ala Glu Asp Val Lys Asn Asp Ser Asn Ala Asn Gln Lys Glu
 145 150 155 160

Val Asp Asp Ala Thr Lys Asn Leu Lys Asn Thr Leu Asn Asn Leu Lys
 165 170 175

Gly Gln Pro Ala Lys Lys Ala Asn Leu Ile Ala Ser Lys Asp Asn Ala
 180 185 190

Lys Ile His Lys Gln Thr Leu Leu Pro Gln Thr Gly Thr Glu Thr Asn
 195 200 205

Pro Leu Thr Ala Ile Gly Ile Gly Leu Met Ala Leu Gly Ala Gly Ile
 210 215 220

Phe Ala
 225

<210> 9
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Streptococcus
 pyogenes M6 (emm6) protein signature cell wall
 sorting signal motif, substrate for sortase-like
 proteins, cell wall anchor motif

 <220>
 <221> MOD_RES
 <222> (3)
 <223> Xaa = any amino acid

 <400> 9
 Leu Pro Xaa Thr Gly
 1 5

 <210> 10
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C-terminus
 positive charged residues cell surface retention
 signal

 <400> 10
 Lys Arg Lys Glu Glu Asn
 1 5

 <210> 11
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:cell wall
 targeting region

 <400> 11
 Leu Pro Gln Ser Gly
 1 5

 <210> 12
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:cell wall
 targeting region

<400> 12
 Leu Pro Gln Ala Gly
 1 5

<210> 13
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:cell wall
 targeting region, cell wall sorting signal, cell
 wall associated (CWA) domain

<400> 13
 Leu Pro Gln Thr Gly
 1 5

<210> 14
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:cell wall
 targeting region

<400> 14
 Leu Pro Gln Thr Ala
 1 5

<210> 15
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:c-Myc epitope,
 c-Myc tag

<400> 15
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
 1 5 10

<210> 16
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C14 C-terminal
 charged tail

<400> 16
 Val Asn Arg Lys Lys Arg Gln Lys
 1 5

<210> 17
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:C370 C-terminal
charged tail

<400> 17
Phe Ala Lys Lys Lys Arg Lys Asp Asp Glu Ala
1 5 10

<210> 18
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:cell wall
sorting signal, cell wall targeting region

<400> 18
Leu Pro Gln Ser Ala
1 5

<210> 19
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:cell wall
sorting signal, cell wall targeting region

<400> 19
Leu Pro Gln Ala Ala
1 5

<210> 20
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:C14 carboxyl
terminus hydrophobic region spanning bacterial
membrane

<400> 20
Val Gly Ile Leu Gly Leu Ala Ile Ala Thr Val Gly Ser Leu Leu Gly
1 5 10 15

Leu Gly Val

<210> 21
<211> 18
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:C370 carboxyl
terminus hydrophobic region spanning bacterial
membrane

<400> 21

Pro Leu Thr Ala Ile Gly Ile Gly Leu Met Ala Leu Gly Ala Gly Ile
1 5 10 15

Phe Ala

<210> 22
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:C191 exemplary
carboxyl terminal positive charged region,
positive charged tails

<400> 22

Lys Lys Arg Lys Glu Asp
1 5

<210> 23
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:C14 exemplary
carboxyl terminal positive charged region,
positive charged tails

<400> 23

Arg Lys Lys Arg Gln Lys
1 5

<210> 24
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:C370 exemplary
carboxyl terminal positive charged region,
positive charged tails

<400> 24

Lys Lys Lys Arg Lys Asp Asp Glu Ala
1 5

<210> 25
 <211> 23
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:exemplary
 signal sequence from amino terminus of
 alpha-amylase of *Lactobacillus amylovorus*

 <400> 25
 Met Lys Lys Asn Leu Arg Ile Val Ser Ala Ala Ala Ala Ala Leu Leu
 1 5 10 15

 Ala Val Ala Pro Val Ala Ala
 20

<210> 26
 <211> 23
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:exemplary
 signal sequence from amino terminus of S-layer
 gene (cbsA) of *Lactobacillus crispatus*

 <400> 26
 Met Lys Lys Asn Leu Arg Ile Val Ser Ala Ala Ala Ala Ala Leu Leu
 1 5 10 15

 Ala Val Ala Thr Val Ser Ala
 20

<210> 27
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Lactobacillus
 paracasei PrtP protease sorting signal

 <400> 27
 Leu Pro Lys Thr Ala
 1 5

<210> 28
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Staphylococcus
 aureus protein A cell wall sorting motif

<400> 28
 Leu Pro Glu Thr Gly
 1 5

<210> 29
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial
 Sequence:Peptostreptococcus magnus protein L and
 human serum albumin binding protein sorting signal
 motif

<220>
 <221> MOD_RES
 <222> (3)
 <223> Xaa = any amino acid

<400> 29
 Leu Pro Xaa Ala Gly
 1 5

<210> 30
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Lactobacillus
 paracasei sorting signal motif

<220>
 <221> MOD_RES
 <222> (3)
 <223> Xaa = any amino acid

<400> 30
 Leu Pro Xaa Thr Ala
 1 5

<210> 31
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Gram-positive
 bacterial cell wall anchored protein conserved
 C-terminal motif

<220>
 <221> MOD_RES
 <222> (1)..(6)
 <223> Xaa = any amino acid

<400> 31
Leu Pro Xaa Thr Gly Xaa
1 5

<210> 32
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification oligonucleotide primer P23.f

<400> 32
gtggagctcc ccgaaaagcc ctgacaaccc 30

<210> 33
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification oligonucleotide primer P23.r

<400> 33
ggaaacacgc tagcactaac ttcatt 26

<210> 34
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification oligonucleotide primer 2DCD4.f

<400> 34
gcggctagca agaaagttgt tttaggtaaa 30

<210> 35
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification oligonucleotide primer 2DCD4.r

<400> 35
gcacaattgt gatgcctttt gaaaagctaa 30

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification oligonucleotide primer CbsAss.f

 <400> 36
 gcgaattcaa ggaggaaaag accacat 27

 <210> 37
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification oligonucleotide primer CbsAss.r

 <400> 37
 ccagctagct gaaacagtag aaacggc 27

 <210> 38
 <211> 59
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:5'
 oligonucleotide primer Myc14nhe

 <400> 38
 gcgctagcga acagaaactg atctccgaag aggacctggt aactcgtact atcaatgta 59

 <210> 39
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:3'
 oligonucleotide primer Myc14mfe

 <400> 39
 cgccaattgc tactttttgac gtttctttct 30

 <210> 40
 <211> 57
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:5'
 oligonucleotide primer Myc191nhe

 <400> 40
 gcgctagcga acagaaactg atctccgaag aggacctgga cgtagtaatt ccaggaa 57

<210> 41
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:3'
 oligonucleotide primer Myc191mfe

 <400> 41
 gcgcaattgt taatcttctt ttctcttctt 30

 <210> 42
 <211> 58
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:5'
 oligonucleotide primer Myc370nhe

 <400> 42
 gcgctagcga acagaaactg atctccgaag aggacctggt gaagaaggca gaagaagt 58

 <210> 43
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:3'
 oligonucleotide primer Myc370mfe

 <400> 43
 ccgcaattgt tatgcttcat catcttttct 30

 <210> 44
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C14 PCR
 amplification 5' primer

 <400> 44
 gcgcaattgg taactcgtac tatcaatgta 30

 <210> 45
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C14 PCR
 amplification 3' primer

<400> 45
 cgctctagat acacaaacta ttttacggtc 30

<210> 46
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C191 PCR
 amplification 5' primer

<400> 46
 gcgcaattgg acgtagtaat tccaggaaca 30

<210> 47
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C191 PCR
 amplification 3' primer

<400> 47
 cgggtctagac caagcaattt atatattgct 30

<210> 48
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C370 PCR
 amplification 5' primer

<400> 48
 gcgcaattga agaaggcaga agaagt 26

<210> 49
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C370 PCR
 amplification 3' primer

<400> 49
 ccgtctagat tatgcttcat catcttttct 30

<210> 50
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:shuttle vector
 cloning primer Mfec14up

 <400> 50
 gcgcaattgc cacaaactgg ttctaagact 30

 <210> 51
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:shuttle vector
 cloning 3' primer Xnac14lo

 <400> 51
 cgctctagat acacaaacta ttttacggtc 30

 <210> 52
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C370 repetitive
 cell wall spanning region zero repeat PCR
 amplification 5' primer

 <400> 52
 cggcaattgc ctcaaactgg tactga 26

 <210> 53
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C370 repetitive
 cell wall spanning region one repeat PCR
 amplification 5' primer

 <400> 53
 cggcaattgg gtcaaactac aaataaagat 30

 <210> 54
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C370 repetitive
 cell wall spanning region two repeat PCR
 amplification 5' primer

 <400> 54
 cgccaattgg gtcaaactac tgataagagt 30

<210> 55
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C370 repetitive
 cell wall spanning region three repeat PCR
 amplification 5' primer

 <400> 55
 gcgcaattgg gtcaaactac aaataaagat 30

 <210> 56
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C370 repetitive
 cell wall spanning region four-eight repeat PCR
 amplification 5' primer

 <400> 56
 cggcaattgg gtcaaactac tgacaagagc 30

 <210> 57
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C14 nucleotide
 sequence corresponding to LPQTG and flanking
 sequences

 <400> 57
 gaaagtaaga agactttacc acaaactggt tctaagactg aa 42

 <210> 58
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C370 nucleotide
 sequence corresponding to LPQTG and flanking
 sequences

 <400> 58
 cataagcaaa ctctattgcc tcaaactggt actgaaacta acccac 46

 <210> 59
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C14
 site-directed mutagenic primer 237P(A)

<400> 59
 gaaagtaaga agactttagc acaaactggg tctaaga 37

<210> 60
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C14
 site-directed mutagenic primer 237P(A)

<400> 60
 gtcttagaac cagtttgtgc taaagtcttc ttactttc 38

<210> 61
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C14
 site-directed mutagenic primer 237P(N)

<400> 61
 gaaagtaaga agactttaaa tcaaactggg tctaagac 38

<210> 62
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C14
 site-directed mutagenic primer 237P(N)

<400> 62
 gtcttagaac cagtttgatt taaagtcttc ttactttc 38

<210> 63
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C14
 site-directed mutagenic primer 237T(A)

<400> 63
 agaagacttt accacaagct gggtctaaga ctgaac 36

<210> 64
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C14
 site-directed mutagenic primer 237T(A)

 <400> 64
 gttcagtctt agaaccagct tgtggtaaag tcttct 36

 <210> 65
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C14
 site-directed mutagenic primer 237T(G)

 <400> 65
 agaagacttt accacaaggt ggttctaaga ctgaac 36

 <210> 66
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C14
 site-directed mutagenic primer 237T(G)

 <400> 66
 gttcagtctt agaaccacct tgtggtaaag tcttct 36

 <210> 67
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C14
 site-directed mutagenic primer 237T(S)

 <400> 67
 agaagacttt accacaaagt ggttctaaga ctgaac 36

 <210> 68
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C14
 site-directed mutagenic primer 237T(S)

<400> 68
 gtttagtttca gtaccacttt gaggcaatag agtttg 36

<210> 69
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C14
 site-directed mutagenic primer 237G(A)

<400> 69
 gactttacca caaactgctt ctaagactga acaag 35

<210> 70
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C14
 site-directed mutagenic primer 237G(A)

<400> 70
 cttgttcagt cttagaagca gtttgtggta aagtc 35

<210> 71
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C370
 site-directed mutagenic primer 249P(A)

<400> 71
 cataagcaaa ctctattggc tcaaactggt actgaaac 38

<210> 72
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C370
 site-directed mutagenic primer 249P(A)

<400> 72
 gtttcagtag cagtttgagc caatagagtt tgcttatg 38

<210> 73
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C370
 site-directed mutagenic primer 249P(N)

 <400> 73
 cataagcaaa ctctattgaa tcaaactggt actgaaac 38

 <210> 74
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C370
 site-directed mutagenic primer 249P(N)

 <400> 74
 gtttcagtagc cagtttgatt caatagagtt tgcttatg 38

 <210> 75
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C370
 site-directed mutagenic primer 249T(A)

 <400> 75
 caaactctat tgcctcaaag tggtagtgaa actaa 35

 <210> 76
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C370
 site-directed mutagenic primer 249T(A)

 <400> 76
 gtttagtttca gtaccagttt gaggcaatag agtttg 36

 <210> 77
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C370
 site-directed mutagenic primer 249T(G)

 <400> 77
 caaactctat tgcctcaagg tggtagtgaa actaac 36

<210> 78
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C370
 site-directed mutagenic primer 249T(G)

 <400> 78
 gttagtttca gtaccacctt gaggcaatag agtttg 36

 <210> 79
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C370
 site-directed mutagenic primer 249T(S)

 <400> 79
 caaactctat tgcctcaaag tggactgaa act 33

 <210> 80
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C370
 site-directed mutagenic primer 249T(S)

 <400> 80
 gttagtttca gtaccacttt gaggcaatag agtttg 36

 <210> 81
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C370
 site-directed mutagenic primer 249G(A)

 <400> 81
 ctctattgcc tcaaactgct actgaaacta acccac 36

 <210> 82
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:C370
 site-directed mutagenic primer 249G(A)

<400> 82
 gtgggttagt ttcagtagca gtttgaggca atagag 36

<210> 83
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:CD4F forward
 amplification primer oligonucleotide

<400> 83
 gatcgtgctg attcacgtcg t 21

<210> 84
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C14-7 reverse
 amplification primer oligonucleotide

<400> 84
 gcgctctaga ctaaacacct aagcctaata agc 33

<210> 85
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C14-6 reverse
 amplification primer oligonucleotide

<400> 85
 gcgctctaga ctagttaaca cctaagccta ataag 35

<210> 86
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:C14-5 reverse
 amplification primer oligonucleotide

<400> 86
 gcgctctaga ctatctgtta acacctaagc c 31

<210> 87
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:370-10 reverse
 amplification primer oligonucleotide

 <400> 87
 gcgctctaga ttaaaaaatt cctgcgcta atg 33

 <210> 88
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:370-9 reverse
 amplification primer oligonucleotide

 <400> 88
 gcgctctaga ttatgcaaaa attcctgcgc ctaatg 36

 <210> 89
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:370-8 reverse
 amplification primer oligonucleotide

 <400> 89
 gcgctctaga ttactttgca aaaattcctg cgcc 34